LISTING OF THE CLAIMS

The following listing of the claims replaces all prior versions and listings of claims for this application. Within the following listing of the claims, claims 1-16 are canceled and claims 17-110 are new.

1-16. **(Canceled)**

17. **(New)** A method of calculating a patient's relative risk (RR) for adverse drug reactions (ADRs) from statin therapy by genotyping a single nucleotide polymorphism (SNP) in DNA of the patient, wherein for three possible genotypes of each SNP, the relative risk associate with each genotype is calculated as follows:

$$RR\ 1 = \frac{N\,11}{N\,21} \Big/ \frac{N\,12 + N\,13}{N\,22 + N\,23}$$

$$RR\ 2 = \frac{N\,12}{N\,22} \Big/ \frac{N\,11 + N\,13}{N\,21 + N\,23}$$

$$RR\ 3 = \frac{N\,13}{N\,23} \Big/ \frac{N\,11 + N\,12}{N\,21 + N\,22}$$

wherein:

RR1 represents the relative risk for genotype 1;

RR2 represents the relative risk for genotype 2;

RR3 represents the relative risk for genotype 3;

N11 represents genotype 1, N12 represents genotype 2, and N13 represents genotype 3 for a population of patients that are being tested for ADRs from statin therapy;

N21 represents genotype 1, N22 represents genotype 2, and N23 represents genotype 3 for a population of patients that are known not to be at risk for ADRs from statin therapy;

a value of RR1 > 1 indicates an increased risk for ADRs from statin therapy for individuals carrying genotype 1;

a value of RR2 > 1 indicates an increased risk for ADRs from statin therapy for individuals carrying genotype 2; and

a value of RR3 > 1 indicates an increased risk for ADRs from statin therapy for individuals carrying genotype 3.

18. **(New)** The method of claim 17, wherein genotype 1, genotype 2, and genotype 3 represent a single nucleotide polymorphism (SNP).

19. **(New)** The method of claim 18, wherein the SNP is a C to T SNP.

20. **(New)** The method of claim 19, wherein genotype 1, genotype 2, and genotype 3 are CC, TT, and CT.

21. **(New)** The method of claim 18, wherein the SNP is an A to G SNP.

22. **(New)** The method of claim 21, wherein genotype 1, genotype 2, and genotype 3 are AA, AG, and GG.

23. **(New)** The method of claim 18, wherein the SNP is a C to G SNP.

24. **(New)** The method of claim 23, wherein genotype 1, genotype 2, and genotype 3 are CC, CG, and GG.

25. **(New)** The method of claim 18, wherein the SNP is an A to T SNP.

26. **(New)** The method of claim 25, wherein genotype 1, genotype 2, and genotype 3 are AA, AT, and TT.

27. **(New)** The method of claim 18, wherein the SNP is a G to T SNP.

28. **(New)** The method of claim 27, wherein genotype 1, genotype 2, and genotype 3 are GG, GT, and TT.

29. **(New)** The method of claim 18, wherein the SNP is an A to C SNP.

30. **(New)** The method of claim 29, wherein genotype 1, genotype 2, and genotype 3 are AA, AC, and CC.

31. **(New)** A method of calculating a patient's relative risk (RR) for adverse drug reactions (ADRs) from statin therapy by determining allele frequency in a single nucleotide polymorphism (SNP) in DNA of the patient, wherein for two possible alleles of each SNP, the relative risk associate with each allele is calculated as follows:

$$RR\ 1 = \frac{N\,11}{N\,21} \Big/ \frac{N\,12}{N\,22}$$

$$RR\ 2 = \frac{N\,12}{N\,22} \Big/ \frac{N\,11}{N\,21}$$

wherein:

RR1 represents the relative risk for allele 1;

RR2 represents the relative risk for allele 2;

N11 represents allele 1 and N12 represents allele 2 for a population of patients that are being tested for ADRs from statin therapy;

N21 represents allele 1 and N22 represents allele 2 for a population of patients that are known not to be at risk for ADRs from statin therapy;

a value of RR1 > 1 indicates an increased risk for ADRs from statin therapy for individuals carrying allele 1; and

a value of RR2 > 1 indicates an increased risk for ADRs from statin therapy for individuals carrying allele 2.

32. **(New)** The method of claim 31, wherein allele 1 and allele 2 are independently selected from A, C, T, and G.

33. **(New)** The method of claim 32, wherein allele 1 and allele 2 are C and T, respectively.

34. **(New)** The method of claim 32, wherein allele 1 and allele 2 are A and G, respectively.

35. **(New)** The method of claim 32, wherein allele 1 and allele 2 are A and T, respectively.

36. **(New)** The method of claim 32, wherein allele 1 and allele 2 are C and G, respectively.

37. **(New)** The method of claim 32, wherein allele 1 and allele 2 are A and C, respectively.

38. **(New)** The method of claim 32, wherein allele 1 and allele 2 are G and T, respectively.

39. **(New)** The method of claims 17 and 31, wherein patients with RR1 < 1, RR2 < 1, or RR3 < 1 should receive low doses of statins or switch to alternative therapies to avoid ADRs.

40. **(New)** A method of calculating a patient's relative risk (RR) for being a high responder to statin therapy by genotyping a single nucleotide polymorphism (SNP) in DNA of the patient, wherein for three possible genotypes of each SNP, the relative risk associate with each genotype is calculated as follows:

$$RR\ 1 = \frac{N\,11}{N\,21} \Big/ \frac{N\,12 + N\,13}{N\,22 + N\,23}$$

$$RR\ 2 = \frac{N\,12}{N\,22} \Big/ \frac{N\,11 + N\,13}{N\,21 + N\,23}$$

$$RR\ 3 = \frac{N\,13}{N\,23} \Big/ \frac{N\,11 + N\,12}{N\,21 + N\,22}$$

wherein:

RR1 represents the relative risk for genotype 1;

RR2 represents the relative risk for genotype 2;

RR3 represents the relative risk for genotype 3;

N11 represents genotype 1, N12 represents genotype 2, and N13 represents genotype 3 for a population of patients that are being tested for high response to statin therapy;

N21 represents genotype 1, N22 represents genotype 2, and N23 represents genotype 3 for a population of patients that are low responders statin therapy;

a value of RR1 > 1 indicates an increased risk for being a high responder to statin therapy for individuals carrying genotype 1;

a value of RR2 > 1 indicates an increased risk for being a high responder to statin therapy for individuals carrying genotype 2; and

a value of RR > 1 indicates an increased risk for being a high responder to statin therapy individuals carrying genotype 3.

41. **(New)** The method of claim 40, wherein genotype 1, genotype 2, and genotype 3 represent a single nucleotide polymorphism (SNP).

42. **(New)** The method of claim 41, wherein the SNP is a C to T SNP.

43. **(New)** The method of claim 42, wherein genotype 1, genotype 2, and genotype 3 are CC, TT, and CT.

44. **(New)** The method of claim 41, wherein the SNP is an A to G SNP.

45. **(New)** The method of claim 44, wherein genotype 1, genotype 2, and genotype 3 are AA, AG, and GG.

46. **(New)** The method of claim 41, wherein the SNP is a C to G SNP.

47. **(New)** The method of claim 46, wherein genotype 1, genotype 2, and genotype 3 are CC, CG, and GG.

48. **(New)** The method of claim 41, wherein the SNP is an A to T SNP.

49. **(New)** The method of claim 48, wherein genotype 1, genotype 2, and genotype 3 are AA, AT, and TT.

50. **(New)** The method of claim 41, wherein the SNP is a G to T SNP.

51. **(New)** The method of claim 50, wherein genotype 1, genotype 2, and genotype 3 are GG, GT, and TT.

52. **(New)** The method of claim 41, wherein the SNP is an A to C SNP.

53. **(New)** The method of claim 52, wherein genotype 1, genotype 2, and genotype 3 are AA, AC, and CC.

54. **(New)** A method of calculating a patient's relative risk (RR) for being a high responder to statin therapy by determining allele frequency in a single nucleotide polymorphism (SNP) in DNA of the patient, wherein for two possible alleles of each SNP, the relative risk associate with each allele is calculated as follows:

$$RR\ 1 = \frac{N\,11}{N\,21} \Big/ \frac{N\,12}{N\,22}$$

$$RR\ 2 = \frac{N\,12}{N\,22} \Big/ \frac{N\,11}{N\,21}$$

wherein:

RR1 represents the relative risk for allele 1;

RR2 represents the relative risk for allele 2;

N11 represents allele 1 and N12 represents allele 2 for a population of patients that are being tested for high response to statin therapy;

N21 represents allele 1 and N22 represents allele 2 for a population of patients that are known to be low responders to statin therapy;

a value of RR1 > 1 indicates an increased risk for being a high responder to statin therapy for individuals carrying allele 1; and

a value of RR2 > 1 indicates an increased risk for being a high responder to statin therapy for individuals carrying allele 2.

55. **(New)** The method of claim 54, wherein allele 1 and allele 2 are independently selected from A, C, T, and G.

56. **(New)** The method of claim 55, wherein allele 1 and allele 2 are C and T, respectively.

57. **(New)** The method of claim 55, wherein allele 1 and allele 2 are A and G, respectively.

58. **(New)** The method of claim 55, wherein allele 1 and allele 2 are A and T, respectively.

59. **(New)** The method of claim 55, wherein allele 1 and allele 2 are C and G, respectively.

60. **(New)** The method of claim 55, wherein allele 1 and allele 2 are A and C, respectively.

61. **(New)** The method of claim 55, wherein allele 1 and allele 2 are G and T, respectively.

62. **(New)** The method of claims 31 and 54, wherein patients with RR1 < 1, RR2 < 1, or RR3 < 1 should receive low doses of statins in order to avoid adverse drug reactions.

63. **(New)** A method of calculating a patient's relative risk (RR) for cardiovascular disease (CVD) by genotyping a single nucleotide polymorphism (SNP) in DNA of the patient, wherein for three possible genotypes of each SNP, the relative risk associate with each genotype is calculated as follows:

$$RR\ 1 = \frac{N11}{N21} \Big/ \frac{N12 + N13}{N22 + N23}$$

$$RR\ 2 = \frac{N12}{N22} \Big/ \frac{N11 + N13}{N21 + N23}$$

$$RR\ 3 = \frac{N13}{N23} \Big/ \frac{N11 + N12}{N21 + N22}$$

wherein:

RR1 represents the relative risk for genotype 1;

RR2 represents the relative risk for genotype 2;

RR3 represents the relative risk for genotype 3;

N11 represents genotype 1, N12 represents genotype 2, and N13 represents genotype 3 for a population of patients that are being tested for CVD;

N21 represents genotype 1, N22 represents genotype 2, and N23 represents genotype 3 for a population of patients that are known not to be at risk for CVD;

a value of RR1 > 1 indicates an increased risk for CVD for individuals carrying genotype 1;

a value of RR2 > 1 indicates an increased risk for CVD for individuals carrying genotype 2; and

a value of RR3 > 1 indicates an increased risk for CVD for individuals carrying genotype 3.

64. **(New)** The method of claim 63, wherein genotype 1, genotype 2, and genotype 3 represent a single nucleotide polymorphism (SNP).

65. **(New)** The method of claim 64, wherein the SNP is a C to T SNP.

66. **(New)** The method of claim 65, wherein genotype 1, genotype 2, and genotype 3 are CC, TT, and CT.

67. **(New)** The method of claim 64, wherein the SNP is an A to G SNP.

68. **(New)** The method of claim 67, wherein genotype 1, genotype 2, and genotype 3 are AA, AG, and GG.

69. **(New)** The method of claim 64, wherein the SNP is a C to G SNP.

70. **(New)** The method of claim 69, wherein genotype 1, genotype 2, and genotype 3 are CC, CG, and GG.

71. **(New)** The method of claim 64, wherein the SNP is an A to T SNP.

72. **(New)** The method of claim 71, wherein genotype 1, genotype 2, and genotype 3 are AA, AT, and TT.

73. **(New)** The method of claim 64, wherein the SNP is a G to T SNP.

74. **(New)** The method of claim 73, wherein genotype 1, genotype 2, and genotype 3 are GG, GT, and TT.

75. **(New)** The method of claim 64, wherein the SNP is an A to C SNP.

76. **(New)** The method of claim 75, wherein genotype 1, genotype 2, and genotype 3 are AA, AC, and CC.

77. **(New)** A method of calculating a patient's relative risk (RR) for cardiovascular disease (CVD) by determining allele frequency in a single nucleotide polymorphism (SNP) in DNA of the patient, wherein for two possible alleles of each SNP, the relative risk associate with each allele is calculated as follows:

$$RR\ 1 = \frac{N\,11}{N\,21} \Big/ \frac{N\,12}{N\,22}$$

$$RR\ 2 = \frac{N\,12}{N\,22} \Big/ \frac{N\,11}{N\,21}$$

wherein:

RR1 represents the relative risk for allele 1;

RR2 represents the relative risk for allele 2;

N11 represents allele 1 and N12 represents allele 2 for a population of patients that are being tested for CVD;

N21 represents allele 1 and N22 represents allele 2 for a population of patients that are known not to be at risk for CVD;

a value of RR1 > 1 indicates an increased risk for CVD for individuals carrying allele 1; and

a value of RR2 > 1 indicates an increased risk for CVD for individuals carrying allele 2.

78. **(New)** The method of claim 77, wherein allele 1 and allele 2 are independently selected from A, C, T, and G.

79. **(New)** The method of claim 78, wherein allele 1 and allele 2 are C and T, respectively.

80. **(New)** The method of claim 78, wherein allele 1 and allele 2 are A and G, respectively.

81. **(New)** The method of claim 78, wherein allele 1 and allele 2 are A and T, respectively.

82. **(New)** The method of claim 78, wherein allele 1 and allele 2 are C and G, respectively.

83. **(New)** The method of claim 78, wherein allele 1 and allele 2 are A and C, respectively.

84. **(New)** The method of claim 78, wherein allele 1 and allele 2 are G and T, respectively.

85. **(New)** The method of claim 19, wherein the C to T SNP is genotyped using oligonucleotide primers of SEQ ID NOs: 157-160 (baySNP 1722); SEQ ID NOs: 181-184 (baySNP 1837); SEQ ID NOs: 197-200 (baySNP 2000); SEQ ID NOs: 321-324 (baySNP 6236); SEQ ID NOs: 325-328 (baySNP 6744); SEQ ID NOs: 365-368 (baySNP 10542); SEQ ID NOs: 397-400 (baySNP 11001); SEQ ID NOs: 401-404 (baySNP 11001)SEQ ID NOs: 413-416 (baySNP 11210); SEQ ID NOs: 417-420 (baySNP 11248); SEQ ID NOs: 453-456 (baySNP 11502); SEQ ID NOs: 469-42 (baySNP 11594); and SEQ ID NOs: 533-536 (baySNP 900107).

86. **(New)** The method of claim 21, wherein the A to G SNP is genotyped using oligonucleotide primers selected from the group consisting of SEQ ID NOs: 5-8 (baySNP 29); SEQ ID NOs: 73-76 (baySNP 542): SEQ ID NOs: 165-168 (baySNP 1765): SEQ ID NOs: 285-288 (baySNP 4966): SEQ ID NOs: 290-292 (baySNP 5014); SEQ ID NOs: 309-312 (baySNP 5717); SEQ ID NOs: 313-316 (baySNP 5959); SEQ ID NOs: 353-356 (baySNP 9698); SEQ ID NOs: 377-380 (baySNP 10745); SEQ ID NOs: 485-488 (baySNP 11654); SEQ ID NOs: 497-500 (baySNP 11825); SEQ ID NOs: 505-508 (baySNP 12097); SEQ ID NOs: 509-512 (baySNP 12366); SEQ ID NOs: 513-516 (baySNP 12619); and SEQ ID NOs: 529-532 (baySNP 900078).

87. **(New)** The method of claim 23, wherein the C to G SNP is genotyped using oligonucleotide primers selected from the group consisting of SEQ ID NOs: 317-320 (baySNP 6162); SEQ ID NOs: 381-384 (baySNP 10771); SEQ ID NOs: 405-408 (baySNP 11073); and SEQ ID NOs: 445-448 (baySNP 11488).

88. **(New)** The method of claim 25, wherein the A to T SNP is genotyped using oligonucleotide primers selected from the group consisting of SEQ ID NOs: 273-276 (baySNP 4206); SEQ ID NOs: 362-364 (baySNP 10481); SEQ ID NOs: 441-444 (baySNP 11487); and SEQ ID NOs: 501-504 (baySNP 11914).

89. **(New)** The method of claim 27, wherein the G to T SNP is genotyped using oligonucleotide primers of SEQ ID NOs: 257-260 (baySNP 3360).

90. **(New)** The method of claim 29, wherein the A to C SNP is genotyped using oligonucleotide primers selected from the group consisting of SEQ ID NOs:129-132 (baySNP 1524); SEQ ID NOs: 253-256 (baySNP 2995) SEQ ID NOs: 489-492 (baySNP 11655); and SEQ ID NOs: 517-520 (baySNP 13025).

91. **(New)** The method of claim 42, wherein the C to T SNP is genotyped using oligonucleotide primers selected from the group consisting of SEQ ID NOs: 1-4 (baySNP 28); SEQ ID NOs: 29-32 (baySNP 140); SEQ ID NOs: 113-116 (baySNP 1101); SEQ ID NOs: 297-300 (baySNP 5298); SEQ ID NOs: 365-268 (baySNP 10542); SEQ ID NOs: 473-476 (baySNP 11624); SEQ ID NOs: 477-480 (baySNP 11627); SEQ ID NOs: 493-496 (baySNP 11656); and SEQ ID NOs: 525-528 (baySNP 900045).

92. **(New)** The method of claim 44, wherein the A to G SNP is genotyped using oligonucleotide primer selected form the group consisting of SEQ ID NOs: 33-36 (baySNP 152); SEQ ID NOs: 69-72 (baySNP 472); SEQ ID NOs: 93-96 (baySNP 1056); SEQ ID NOs: 161-164 (baySNP 1757); SEQ ID NOs: 177-180 (baySNP 1806); SEQ ID NOs: 217-220 (baySNP 2119); SEQ ID NOs: 221-224 (baySNP 2141); SEQ ID NOs: (baySNP 3976269-272); SEQ ID NOs: 277-280 (baySNP 4912); SEQ ID NOs: 293-296 (baySNP 5296); SEQ ID NOs: 301-304 (baySNP 5457); SEQ ID NOs: 333-336 (baySNP 8210); SEQ ID NOs: 369-372 (baySNP 10600); SEQ ID NOs: 377-380 (baySNP 10745); SEQ ID NOs: 461-464 (baySNP 11537); SEQ ID NOs: 465-468 (baySNP 11560); SEQ ID NOs: 481-484 (baySNP 11650); SEQ ID NOs: 509-512 (baySNP 12366); and SEQ ID NOs: 537-540 (baySNP 10000002).

93. **(New)** The method of claim 46, wherein the C to G SNP is genotyped using oligonucletoide primers selected from the group consisting of SEQ ID NOs: 9-12 (baySNP 52); SEQ ID NOs: 13-16 (baySNP 56); SEQ ID NOs: 133-136 (baySNP 1556); SEQ ID NOs: 381-384 (baySNP 10771); SEQ ID NOs: 445-448 (baySNP 11488).

94. **(New)** The method of claim 48, wherein the A to T SN P is genotyped using oligonucleotide primers of SEQ ID NOs: 429-432 (baySNP 11450).

95. **(New)** The method of claim 50, wherein the G to T SNP is genotyped using oligonucleotide primers selected from SEQ ID NOs: 125-128 (baySNP 1511) and SEQ ID NOs: 209-212 (baySNP 2085).

96. **(New)** The method of claim 52, wherein the A to C SNP is genotyped using oligonucleotide primers selected from the group consisting of SEQ ID NOs: 81-84 (baySNP 821); SEQ ID NOs: 233-236 (baySNP 2281); SEQ ID NOs: 253-256 (baySNP 2995); and SEQ ID NOs: 265-268 (baySNP 3975).

97. **(New)** The method of claim 65, wherein the C to T SNP is genotyped using oligonucleotide primers selected from the group consisting of SEQ ID NOs: 21-24 (baySNP 90); SEQ ID NOs: 25-28 (baySNP 99); SEQ ID NOs: 45-48 (baySNP 224); SEQ ID NOs: 49-52 (baySNP 294); SEQ ID NOs: 53-56 (baySNP 307); SEQ ID NOs: 65-68 (baySNP 466); SEQ ID NOs: 121-124 (baySNP 1504); SEQ ID NOs: 141-144 (baySNP 1582); SEQ ID NOs: 149-152 (baySNP 1662); SEQ ID NOs: 173-176 (baySNP 1799); SEQ ID NOs: 181-184 (baySNP 1837); SEQ ID NOs: 185-188 (baySNP 1870); SEQ ID NOs: 189-192 (baySNP 1882); SEQ ID NOs: 193-196 (baySNP 1988); SEQ ID NOs: 197-200 (baySNP 2000); SEQ ID NOs: 241-244 (baySNP 2341); SEQ ID NOs: 297-300 (baySNP 5298); SEQ ID NOs: 305-308 (baySNP 5704); SEQ ID NOs: 373-376 (baySNP 10621); SEQ ID NOs: 409-412 (baySNP 11153); SEQ ID NOs: 413-415 (baySNP 11210); SEQ ID NOs: 417-420 (baySNP 11248); SEQ ID NOs: 433-436 (baySNP 11470); SEQ ID NOs: 473-476 (baySNP 11624); SEQ ID NOs: 477-480 (baySNP 11627); SEQ ID NOs: 493-396 (baySNP 11656); and SEQ ID NOs: 549-552 (baySNP 10000025).

98. **(New)** The method of claim 67, wherein the A to G SNP is genotyped using oligonucleotide primers selected from the group consisting of SEQ ID NOs: 5-8 (baySNP 29); SEQ ID NOs: 17-20 (baySNP 89); SEQ ID NOs: 37-40 (baySNP 214); SEQ ID NOs: 73-76 (baySNP 542); SEQ ID NOs: 85-88 (baySNP 1005); SEQ ID NOs: 97-100 (baySNP 1085); SEQ ID NOs: 101-104 (baySNP 1086); SEQ ID NOs: 117-120 (baySNP 1204); SEQ ID NOs: 144-148 (baySNP 1638); SEQ ID NOs: 153-156 (baySNP 1714); SEQ ID NOs: 169-172 (baySNP 1776); SEQ ID NOs: 201-204 (baySNP 2071); SEQ ID NOs: 213-216 (baySNP 2095); SEQ ID NOs: 217-220 (baySNP 2119); SEQ ID NOs: 221-224 (baySNP 2141); SEQ ID NOs: 245-248 (baySNP 2357); SEQ ID NOs: 261-264 (baySNP 3464); SEQ ID NOs: 293-296 (baySNP 5296); SEQ ID NOs: 313-316 (baySNP 5959); SEQ ID NOs: 349-352 (baySNP 9516); SEQ ID NOs: 353-356 (baySNP 9698); SEQ ID NOs: 357-360 (baySNP 9883); SEQ ID NOs: 385-388 (baySNP 10870); SEQ ID NOs: 421-424 (baySNP 11372); SEQ ID NOs: 449-452 (baySNP 11493); SEQ ID NOs: 461-464 (baySNP 11537); and SEQ ID NOs: 541-544 (baySNP 10000006).

99. **(New)** The method of claim 69, wherein the C to G SNP is genotyped with oligonucleotide primers selected from the group consisting of SEQ ID NOs: 41-44 (baySNP 221); SEQ ID NOs: 61-64 (baySNP 449); SEQ ID NOs: 77-80 (baySNP 739); SEQ ID NOs: 105-108 (baySNP 1092); SEQ ID NOs: 329-332 (baySNP 7133); SEQ ID NOs: 345-348 (baySNP 9193); and SEQ ID NOs: 425-428 (baySNP 11449).

100. **(New)** The method of claim 71, wherein the A to T SNP is genotyped with oligonucleotide primers selected from the group consisting of SEQ ID NOs: 57-60 (baySNP 411); SEQ ID NOs: 93-96 (baySNP 1055); and SEQ ID NOs: 436-440 (baySNP 11472).

101. **(New)** The method of claim 73, wherein the G to T SNP is genotyped with oligonucleotide primers selected from the group consisting of SEQ ID NOs: 109-112 (baySNP 1096); SEQ ID NOs: 205-208 (baySNP 2078); SEQ ID NOs: 229-232 (baySNP 2234); SEQ ID NOs: 249-252 (baySNP 2366); SEQ ID NOs: 393-396 (baySNP 10948); and SEQ ID NOs: 457-460 (baySNP 11534).

102. **(New)** The method of claim 75, wherein the A to C SNP is genotyped with oligonucleotide primers selected from the group consisting of SEQ ID NOs: 81-84 (baySNP 821); SEQ ID NOs: 137-140 (baySNP 1561); SEQ ID NOs: 237-240 (baySNP 2298); SEQ ID NOs: 281-284 (baySNP 4925); SEQ ID NOs: 341-344 (baySNP 8943); SEQ ID NOs: 389-392 (baySNP 10877); and SEQ ID NOs: 545-548 (baySNP 10000014).

103. **(New)** The method of claims 19 and 42, wherein the C to T SNP is used to concurrently determine the patient's risk for ADRs from statin therapy and the patient's risk of being a high responder to statin therapy, wherein the C to T SNP is genotyped using oligonucleotide primers of SEQ ID NOs: 365-368 (baySNP 10542).

104. **(New)** The method of claims 19 and 65, wherein the C to T SNP is used to concurrently determine the patient's risk for ADRs from statin therapy and the patient's risk for CVD, wherein the C to T SNP is genotyped with oligonucleotide primers selected from SEQ ID NOs: 181-184 (baySNP 1837); SEQ ID NOs: 197-200 (baySNP 2000); SEQ ID NOs: 417-420 (baySNP 11248); and SEQ ID NOs: 469-472 (baySNP 11594).

105. **(New)** The method of claim 42 and 65, wherein the C to T SNP is used to concurrently determine the patient's risk for being a high responder to statin therapy and the patient's risk for CVD, wherein the C to T SNP is genotyped with oligonucleotide primers selected from SEQ ID NOs: 297-300 (baySNP 5298); SEQ ID NOs: 473-476 (baySNP 11624); SEQ ID NOs: 477-480 (baySNP 11627); and SEQ ID NOs:493-496 (baySNP 11656).

106. **(New)** The method of claims 21 and 44, wherein the A to G SNP is used to concurrently determine the patient's risk for ADRs from statin therapy and the patient's risk of being a high responder to statin therapy, wherein the A to G SNP is genotyped with oligonucleotide primers selected from SEQ ID NOs: 353-356 (baySNP 9698); SEQ ID NOs: 377-380 (baySNP 10745); and SEQ ID NOs: 509-512 (baySNP12366).

107. **(New)** The method of claims 21 and 67, wherein the A to G SNP is used to concurrently determine the patient's risk for ADRs from statin therapy and for the patient's risk for CVD, wherein the A to G SNP is genotyped with oligonucleotide primers selected from SEQ ID NOs: 5-8 (baySNP 29) and SEQ ID NOs: 313-316 (baySNP 5959).

108. **(New)** The method of claims 44 and 67, wherein the A to G SNP is used to concurrently determine the patient's risk for being a high responder to statin therapy and the patient's risk for CVD, wherein the A to G SNP is genotyped with oligonucleotide primers selected from SEQ ID NOs: 217-220 (baySNP 2119); SEQ ID NOs: 221-224 (baySNP 2141); SEQ ID NOs: 293-296 (baySNP 5296); and SEQ ID NOs: 461-464 (baySNP 11537).

109. **(New)** The method of claims 52 and 75, wherein the A to C SNP is used to concurrently determine the patient's risk for being a high responder to statin therapy and for CVD, wherein the A to C SNP is genotyped using oligonucleotide primers of SEQ ID NOs: 81-84 (baySNP 821).

110. **(New)** The method of claims 23 and 46, wherein the C to G SNP is used concurrently determine the patient's risk for ADRs from statin therapy and the patient's risk of being a high responder to statin therapy, wherein the C to G SNP is genotyped using oligonucleotide primers of SEQ ID NOs: 445-448 (baySNP 11488).